

2008-01-09 0760-0354PUS1  
SEQUENCE LISTING

<110> UCHIDA, Yoshiaki  
FUJII, Nobuyuki  
KURANO, Yoshihiro  
OKADA, Masahisa  
KOGAKI, Hiroyuki  
KIDO, Yasuji

<120> ANTI-SARS VIRUS ANTIBODY, HYBRIDOMA PRODUCING THE  
ANTIBODY AND IMMUNOASSAY REAGENT USING THE ANTIBODY

<130> 0760-0354PUS1

<140> US 10/577,310

<141> 2006-04-28

<150> PCT/JP2004/016099

<151> 2004-10-29

<150> JP 2003-373779

<151> 2003-10-31

<150> JP 2004-034268

<151> 2004-02-10

<160> 3

<170> PatentIn version 3.1

<210> 1

<211> 1269

<212> DNA

<213> Coronavirus

<220>

<221> CDS

<222> (1)..(1269)

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aca	ttt	ggt	gga	ccc	aca	gat	tca	act	gac	aat	aac	cag	aat	gga	gga	96
Thr	Phe	Gly	Gly	Pro	Thr	Asp	Ser	Thr	Asp	Asn	Asn	Gln	Asn	Gly	Gly	
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cgc	aat	ggg	gca	agg	cca	aaa	cag	cgc	cga	ccc	caa	ggt	tta	ccc	aat	144
Arg	Asn	Gly	Ala	Arg	Pro	Lys	Gln	Arg	Arg	Pro	Gln	Gly	Leu	Pro	Asn	
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aat	act	gcg	tct	tgg	ttc	aca	gct	ctc	act	cag	cat	ggc	aag	gag	gaa	192
Asn	Thr	Ala	Ser	Trp	Phe	Thr	Ala	Leu	Thr	Gln	His	Gly	Lys	Glu	Glu	
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ctt	aga	ttc	cct	cga	ggc	cag	ggc	gtt	cca	atc	aac	acc	aat	agt	ggt	240
Leu	Arg	Phe	Pro	Arg	Gly	Gln	Gly	Val	Pro	Ile	Asn	Thr	Asn	Ser	Gly	
65					70				75						80	

cca	gat	gac	caa	att	ggc	tac	tac	cga	aga	gct	acc	cga	cga	gtt	cgt	288
Pro	Asp	Asp	Gln	Ile	Gly	Tyr	Tyr	Arg	Arg	Ala	Thr	Arg	Arg	Val	Arg	
				85					90					95		

ggt Gly	ggt Gly	gac Asp	ggc Gly 100	aaa Lys	atg Met	aaa Lys	gag Glu 105	ctc Leu 105	agc Ser	ccc Pro	aga Arg	tgg Trp 110	tac Tyr 110	ttc Phe	tat Tyr	336
tac Tyr	cta Leu	gga Gly 115	act Thr	ggc Gly	cca Pro	gaa Glu	gct Ala 120	tca Ser	ctt Leu	ccc Pro	tac Tyr	ggc Gly 125	gct Ala	aac Asn	aaa Lys	384
gaa Glu	ggc Gly 130	atc Ile	gta Val	tgg Trp	gtt Val	gca Ala 135	act Thr	gag Glu	gga Gly	gcc Ala	ttg Leu 140	aat Asn	aca Thr	ccc Pro	aaa Lys	432
gac Asp 145	cac His	att Ile	ggc Gly	acc Thr	cgc Arg 150	aat Asn	cct Pro	aat Asn	aac Asn	aat Asn 155	gct Ala	gcc Ala	acc Thr	gtg Val	cta Leu 160	480
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cta Leu 225	gac Asp	aga Arg	ttg Leu	aac Asn	cag Gln 230	ctt Leu	gag Glu	agc Ser	aaa Lys	gtt Val 235	tct Ser	ggc Gly	aaa Lys	ggc Gly	caa Gln 240	720
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caa Gln	gca Ala	ttt Phe 275	ggg Gly	aga Arg	cgt Arg	ggt Gly	cca Pro 280	gaa Glu	caa Gln	acc Thr	caa Gln	gga Gly 285	aat Asn	ttc Phe	ggg Gly	864
gac Asp	caa Gln 290	gac Asp	cta Leu	atc Ile	aga Arg	caa Gln 295	gga Gly	act Thr	gat Asp	tac Tyr	aaa Lys 300	cat His	tgg Trp	ccg Pro	caa Gln	912
att Ile 305	gca Ala	caa Gln	ttt Phe	gct Ala	cca Pro 310	agt Ser	gcc Ala	tct Ser	gca Ala	ttc Phe 315	ttt Phe	gga Gly	atg Met	tca Ser	cgc Arg 320	960
att Ile	ggc Gly	atg Met	gaa Glu	gtc Val 325	aca Thr	cct Pro	tcg Ser	gga Gly	aca Thr 330	tgg Trp	ctg Leu	act Thr	tat Tyr	cat His 335	gga Gly	1008
gcc Ala	att Ile	aaa Lys	ttg Leu	gat Asp	gac Asp	aaa Lys	gat Asp	cca Pro	caa Gln	ttc Phe	aaa Lys	gac Asp	aac Asn	gtc Val	ata Ile	1056

340

345

350

ctg	ctg	aac	aag	cac	att	gac	gca	tac	aaa	aca	ttc	cca	cca	aca	gag	1104
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		355					360					365				
cct	aaa	aag	gac	aaa	aag	aaa	aag	act	gat	gaa	gct	cag	cct	ttg	ccg	1152
Pro	Lys	Lys	Asp	Lys	Lys	Lys	Lys	Thr	Asp	Glu	Ala	Gln	Pro	Leu	Pro	
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cag	aga	caa	aag	aag	cag	ccc	act	gtg	act	ctt	ctt	cct	gcg	gct	gac	1200
Gln	Arg	Gln	Lys	Lys	Gln	Pro	Thr	Val	Thr	Leu	Leu	Pro	Ala	Ala	Asp	
385					390					395					400	
atg	gat	gat	ttc	tcc	aga	caa	ctt	caa	aat	tcc	atg	agt	gga	gct	tct	1248
Met	Asp	Asp	Phe	Ser	Arg	Gln	Leu	Gln	Asn	Ser	Met	Ser	Gly	Ala	Ser	
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gct	gat	tca	act	cag	gca	taa										1269
Ala	Asp	Ser	Thr	Gln	Ala											
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Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn  
 35 40 45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu  
 50 55 60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly  
 65 70 75 80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg  
 85 90 95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr  
 100 105 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys  
 115 120 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys  
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135

140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu  
 145 150 155 160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly  
 165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg  
 180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro  
 195 200 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu  
 210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln  
 225 230 235 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser  
 245 250 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr  
 260 265 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly  
 275 280 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln  
 290 295 300

Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg  
 305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly  
 325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile  
 340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu  
 355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro  
 370 375 380

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Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp  
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Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser  
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Ala Asp Ser Thr Gln Ala  
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Arg Cys